

ALIGNMENTS

FEATURES	LOCATION/Qualifiers
BASE COUNT	139 a 106 c 134 g 87 t
ORIGIN	XhoI
Alignment Scores:	
Pred. No.:	1,156-40
Score:	577.00
Percent Similarity:	99.19%
Best Local Similarity:	99.19%
Query Match:	87.29%
DB:	9
Gaps:	0
US-09-866-582A-2 (1-135) x AV392837 (1-466)	
QY	1 Metaspalavalasparglyvaltrpheaapgluaapphenisvalarglileuas
Db	98 ATGACGGCGGTAGATAGAGAGAGTCACTTTGACGAGAGACTTCATGTCCTCCATCTTGAT
QY	21 Valaaplytysrasalaserlyserleuglnaspaenthrasvalphellensn
Db	158 GTTGCAAGTACAAATGCTTCAAGTCGCTCCAGGACACACAAATGTTTCAATTAACAC
QY	41 lleglnasmetglnglyleuvalaspstytyvalaseralaleaspnglnvalglu
Db	218 ATCCAAATATGCAAGCGCTCGTGACAAATAGCTGCCCATGCACAGAGTTCAG
QY	61 Argleugluaglulysleulysalilectglyleuatgsanargvalalaleu
Db	278 CGGCTAGAGAGTGAAGAAAGCTAAGGCCATTGGCTGCGGAACCGGCTGCTCGT
QY	81 Glugluatrglyatrglyglnlysglucglnluatrgmetleuaglulysglnlu
Db	338 GAGGAGCGGAAACGTAAACAAAGAGGAGGAGCCATGCTTAGCGGAGACAGAGAG
QY	101 leugluatrgleuglnmetgluglucglnserleuilelyvallysglyglnlu
Db	398 CTTGAGAGGCTCCAAATGAGAGAGAGTGGTATCAG-GrGAAAGCGGACAGAGCTC
QY	121 Metilegln 123
Db	457 ATGATTTCAG 465
RESULT 2	
BE352290/c	493 bp mRNA linear EST 18-JUL-2000
LOCUS	894059C02.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
DEFINITION	Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION	BE352290
VERSION	BE352290.1 GI:9264143
KEYWORDS	EST.
SOURCE	Chlamydomonas reinhardtii
ORGANISM	Chlamydomonas reinhardtii
REFERENCE	Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
AUTHORS	Chlamydomonadaceae; Chlamydomonas.
TITLE	1 (bases 1 to 493)
JOURNAL	Grossman, A., Davies, J., Pederspiel, N., Harris, E., Lefebvre, P.,
COMMENT	McGermott, J. P., Sillflow, C., Stern, D. and Surzycki, R.
	Analyses of the Chlamydomonas reinhardtii Genome: A Model,
	Unicellular System for Analysing Gene Function and Regulation in
	Vascular Plants: Project phase 2
	Unpublished
	Contact: Elizabeth H. Harris
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	Duke University
	Durham, NC 27708-1000, USA
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	Email: chlamy@duke.edu.

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source
1. 493
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3053"
/clone_lib="C. reinhardtii CC-1690, normalized, lambda Zap
II"
/note="Vector: pBluescript II SK-; Site-1: EcoRI; Site-2:
XhoI. This library, constructed by John Davies and Jeffery
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in YAP (acetate-containing) medium in the
light, YAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
Zap clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      88 a      182 c      101 g      122 t
ORIGIN
Alignment Scores:
Pred. No.:      1.76e-10      Length:      493
Percent Similarity: 227.00      Matches:      48
Best Local Similarity: 100.00%      Conservative: 0
Query Match:      100.00%      Mismatches: 0
DB:      34.34%      Indels:      0
      10      Gaps:      0
US-09-866-582A-2 (1-135) x BE352290 (1-493)
Oy      88      LysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGlnArgLeuGlnMetCln 107
      |||||||
Db      493      AAGGACGAGGAGGCGCATGCTAGCGGAGAGACAGAGGAGCGCTTGAGAGGCTCCCAATGTGAG 434
Oy      108      GluGlnSerLeuLeuLeuValLysGlyGluGlnGlnLeuLeuMetIleGlnLysLeuSerAsp 127
      |||||||
Db      433      GAGCAGTCGCTGATCAAGGTGMAAGGGCGGACGACGACTCATGATTCAAGAGCTGTGGGAC 374
Oy      128      SerSerSerGlyAlaAlaItyrVal 135
      |||||||
Db      373      AGCAGCAGCGGGCGGCGCATACGTG 350
RESULT 3
BM280429      646 bp      mRNA      linear      EST 11-NOV-2002
LOCUS      BM280429
DEFINITION      Intestinalis cDNA clone c1gdd013n23 5', mRNA sequence.
ACCESSION      BM280429
VERSION      BM280429.1 GI:24861040
SOURCE      EST.
ORGANISM      Clona intestinalis
Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Clona.
1 (bases 1 to 646)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@escidlan.zool.kyoto-u.ac.jp.
Unpublished
Contact: Nori Satoh
Department of Zoology,
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Location/Qualifiers
1. 646
/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
FEATURES
source

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BASE COUNT	223	a	107	c	121	g	194	t	1	others
ALIGNMENT SCORES:										
Pred. NO.:	3	12e-08	Length:	646						
Score:	202.00	Matches:	41							
Percent Similarity:	61.48%	Conservative:	34							
Best Local Similarity:	33.61%	Mismatches:	47							
Query Match:	30.56%	Indels:	0							
DB:	13	Gaps:	0							
US-09-866-582a-2 (1-135) x BW280429 (1-646)										
Qy	7	GLYVALTYRHPASPGIUAAPRHEHISVALARGILEUVAAPVALASPLYTRYASNALIA	26							
Db	63	GCGCTCATTTTGACAGAAATTAAACAACCTGCAAGTTTAAACCCAGCACTAATCAGCAC	122							
Qy	27	SerlysserLeuglinasparitthAsnValPheIleasnSnIleclinasmeugIngly	46							
Db	123	ACATCTGAACTGAAAGAGGAATGCCACGAATTCGTCGAAATCGACCGAGTTTCANAAA	182							
Qy	47	LeuValAsplysTryValSerValIleAspCInclnValGluArgLeuGluAgluIlys	66							
Db	183	CTTGTTGGTAGCTTCATGAGATGACATGACCCAGCCATCCGAAAAGATGTTGAAATGAGAA	242							
Qy	67	LeuLYSAIAlIeGlyLeuArgAsnArgValAlaIleAsnSerGluArgIlysArgIlys	86							
Db	243	ATGAAGCCATCGGTTCTCTACATGCTCAAGTCAATTCGACAGCAGAGGAATCCAC	302							
Qy	87	GluIysGluIngluArgMetLeuAlaGluIysGluIngluLeuGluArgLeuGluMet	106							
Db	303	CACAACAGTTGAAAGCAGCATATGCGGAGAAACACAACTTGAGCGATTGAATGTG	362							
Qy	107	GluGluGluInserLeuIleIysValIysGlyGluIngluIleuMetIleGluIlysLeuSer	126							
Db	363	CACACCACTCTCTAAGAAACAGAGGCTGACACAGTTGAATTCATTCAGCAATTCCTCA	422							
Qy	127	AspSer	128							
Db	423	ACTTC	428							
RESULT 4										
BW280674										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
TITLE										
JOURNAL										
COMMENT										
FEATURES										
source										